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MEETING ABSTRACT Open Access

COSMOS: cloud enabled NGS analysis

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Background

The dramatic fall of next generation sequencing (NGS) cost in recent years positions the price in range of typical medical testing, and thus whole genome analysis (WGA) may be a viable clinical diagnostic tool. Modern sequencing platforms routinely generate petabyte data. The current challenge lies in calling and analyzing this large-scale data, which has become the new time and cost rate-limiting step.

Methods

To address the computational limitations and optimize the cost, we have developed COSMOS (http://cosmos.hms.harvard.edu) , a scalable, parallelizable workflow management system running on clouds (e.g., Amazon Web Services or Google Clouds). Using COSMOS [1], we have constructed a NGS analysis pipeline implementing the Genome Analysis Toolkit - GATK v3.1 - best practice protocol [2,3], a widely accepted industry standard developed by the Broad Institute. COSMOS performs a thorough sequence analysis, including quality control, alignment, variant calling and an unprecedented level of annotation using a custom extension of ANNOVAR. COSMOS takes advantage of parallelization and the resources of a high-performance compute cluster, either local or in the cloud, to process datasets of up to the petabyte scale, which is becoming standard in NGS.

Conclusion

This approach enables the timely and cost-effective implementation of NGS analysis, allowing for it to be used in a clinical setting and translational medicine. With COSMOS we reduced the whole genome data analysis cost under the $100 barrier, placing it within a reimbursable cost point and in *clinical time*, providing a significant change to the landscape of genomic analysis and cement the utility of cloud environment as a resource for Petabyte-scale genomic research.

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